

Copyright (c) 1993 - 2000 Compugen Ltd.

GeneCore Version 4.5

OM nucleic - nucleic search, using sw model

Run on: November 9, 2001, 09:08:03 ; Search time 997.13 seconds
 (without alignments)
 15746.382 Million cell updates/sec

Title:	US-09-001-737-7
Perfect score:	1661
Sequence:	1 GATTCGGCTCATATGGCA.....TGGGGCGATAAGCCGAATTC 1661
Scoring table:	IDENTITY_NUC
Gapop 10.0 , Gapext 1.0	
Searched:	10228115 seqs, 4726426750 residues
Total number of hits satisfying chosen parameters:	20456230
Minimum DB seq length: 0	
Maximum DB seq length: 200000000	
Post-processing: Minimum Match 0%	
Listing first 45 summaries	
Database :	
EST: *	
1: gb_est1: *	
2: gb_est2: *	
3: gb_est3: *	
4: gb_est4: *	
5: gb_est5: *	
6: gb_est6: *	
7: gb_est7: *	
8: gb_est8: *	
9: gb_est9: *	
10: gb_est10: *	
11: gb_est11: *	
12: gb_est12: *	
13: gb_est13: *	
14: gb_est14: *	
15: gb_est15: *	
16: gb_est16: *	
17: gb_est17: *	
18: gb_est18: *	
19: gb_est19: *	
20: gb_est20: *	
21: gb_est21: *	
22: gb_est22: *	
23: gb_est23: *	
24: gb_est24: *	
25: gb_est25: *	
26: gb_est26: *	
27: gb_est27: *	
28: gb_est28: *	
29: gb_est29: *	
30: gb_est30: *	
31: gb_est31: *	
32: gb_est32: *	
33: em_estba: *	
34: em_estfun: *	
35: em_esthml: *	
36: em_esthml2: *	
37: em_esthml3: *	
38: em_esthml4: *	
39: em_esthml5: *	
40: em_esthml6: *	
41: em_esthml7: *	
42: em_esthml8: *	
43: em_esthml9: *	
44: em_esthml0: *	
45: em_esthml1: *	
46: em_esthml2: *	
47: em_esthml3: *	
48: em_esthml4: *	
49: em_esthml5: *	
50: em_esthml6: *	
51: em_esthml7: *	
52: em_esthml8: *	
53: em_esthml9: *	
54: em_esthml0: *	
55: em_esthml1: *	
56: em_esthml2: *	
57: em_esthml3: *	
58: em_esthml4: *	
59: em_esthml5: *	
60: em_esthml6: *	
61: em_esthml7: *	
62: em_esthml8: *	
63: em_esthml9: *	
64: em_estin1: *	
65: em_estin2: *	
66: em_estin4: *	
67: em_estin5: *	
68: em_estinm1: *	
69: em_esteem2: *	
70: em_esteem1: *	
71: em_esteemv1: *	
72: em_esteemv11: *	
73: em_esttp12: *	
74: em_esttp13: *	
75: em_esttp14: *	
76: em_esttp15: *	
77: em_esttp16: *	
78: em_esttp17: *	
79: em_esttp18: *	
80: em_esttp19: *	
81: em_esttp10: *	
82: em_esttp11: *	
83: em_estro1: *	
84: em_estro2: *	
85: em_estro3: *	
86: em_estro4: *	
87: em_estro5: *	
88: em_estro6: *	
89: em_estro7: *	
90: em_estro8: *	
91: em_estro9: *	
92: em_estro10: *	
93: em_estro12: *	
94: em_estro13: *	
95: em_estro14: *	
96: em_estro15: *	
97: em_estro16: *	
98: em_estro17: *	
99: em_estro18: *	
100: em_estro19: *	
101: em_estro20: *	
102: gb_est26: *	
103: gb_est25: *	
104: gb_est27: *	
105: gb_est28: *	
106: gb_est29: *	
107: gb_est30: *	
108: gb.est31: *	
109: gb.est22: *	
110: gb.est21: *	
111: gb.est23: *	
112: gb.est43: *	
113: gb.est44: *	
114: gb.est45: *	
115: gb.est46: *	

```

117: gb_est48;*
118: gb_est49;*
119: gb_est50;*
120: gb_est51;*
121: gb_est52;*
122: gb_est53;*
123: gb_est54;*
124: gb_est55;*
125: gb_est56;*
126: gb_est57;*
127: gb_est58;*
128: gb_est59;*
129: gb_est60;*
130: gb_est61;*
131: gb_est62;*
132: gb_est63;*
133: gb_est64;*
134: gb_est65;*
135: gb_est66;*
136: gb_est67;*
137: gb_est68;*
138: gb_est69;*
139: gb_est70;*
140: gb_est71;*
141: gb_est72;*
142: gb_est73;*
143: gb_est74;*
144: gb_est75;*
145: gb_est76;*
146: gb_est77;*
147: gb_est78;*
148: gb_est79;*
149: gb_est80;*
150: gb_est81;*
151: gb_est82;*
152: gb_est83;*
153: gb_est84;*
154: gb_est85;*
155: gb_est86;*
156: gb_est87;*
157: gb_est88;*
158: gb_est89;*
159: gb_est90;*
160: gb_est91;*
161: gb_est92;*
162: gb_est93;*
163: gb_est94;*
164: gb_est95;*
165: gb_est96;*
166: gb_est97;*
167: gb_est98;*
168: gb_est99;*
169: gb_est100;*
170: gb_est101;*
171: gb_est102;*
172: gb_est103;*
173: gb_est104;*
174: gb_est105;*
175: gb_est106;*
176: gb_est107;*
177: gb_est108;*
178: gb_est109;*
179: gb_est110;*
180: gb_est111;*
181: gb_est112;*
182: gb_est113;*
183: gb_est114;*
184: gb_est115;*
185: gb_est116;*
186: gb_est117;*
187: gb_est118;*
188: gb_est119;*
189: gb_est120;*
190: gb_est110;*
191: gb_est111;*
192: gb_htc;*
193: em_gss_fun;*
194: em_gss_hum1;*
195: em_gss_hum2;*
196: em_gss_hum3;*
197: em_gss_hum4;*
198: em_gss_hum5;*
199: em_gss_hum6;*
200: em_gss_hum7;*
201: em_gss_hum8;*
202: em_gss_hum9;*
203: em_gss_invi;*
204: em_gss_invz;*
205: em_gss_inva;*
206: em_gss_other;*
207: em_gss_r0d1;*
208: em_gss_r0d2;*
209: em_gss_r0d3;*
210: em_gss_r0d4;*
211: em_gss_r0d5;*
212: em_gss_r0d6;*
213: em_gss_r0d7;*
214: em_gss_r0d8;*
215: em_gss_vrt1;*
216: em_gss_r0d9;*
217: em_gss_vrt3;*
218: gb_gss1;*
219: gb_gss2;*
220: gb_gss3;*
221: gb_gss4;*
222: gb_gss5;*
223: gb_gss6;*
224: gb_gss7;*
225: gb_gss8;*
226: gb_gss9;*
227: gb_gss10;*
228: gb_gss11;*
229: gb_gss12;*
230: gb_gss13;*
231: gb_gss14;*
232: gb_gss15;*
233: gb_gss16;*
234: gb_gss17;*
235: gb_gss18;*
236: gb_gss19;*
237: gb_gss20;*
238: gb_gss21;*
239: gb_gss22;*
240: gb_gss23;*
241: gb_gss24;*
242: gb_gss25;*
243: gb_gss26;*
244: gb_gss27;*
245: gb_gss28;*
246: gb_gss29;*
247: gb_gss30;*
248: gb_gss31;*
249: gb_gss32;*
250: gb_gss33;*
251: gb_gss34;*
252: em_gss_inva;*
253: em_gss_r0d;*
254: em_gss_r0d1;*
255: em_gss_r0d2;*
256: gb_gss35;*
257: gb_gss36;*
258: gb_gss37;*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	SUMMARIES		JOURNAL COMMENT	
					Description	FEATURES source		
1	261.8	15..8	878	146	BF275584	Unpublished (2000)	of the cotton fiber	
2	257.3	15..5	1035	105	AL518632	Clemson University Genomics Institute	Contact: Wling RA	
3	254	15..3	977	152	BG21293	100 Jordan Hall, Clemson, SC 29634, USA	Tel: 864 655 7288	
4	253.4	15..3	988	106	AL532233	Fax: 864 656 4233	Email: rwing@clemson.edu	
5	249.6	15..0	811	151	BFG24379	Seq printer: TAATACGACTCACTATAAGGG	High quality sequence stop: T 16.	
6	249.6	15..0	1017	105	AL515579	/organism="Gossypium arboreum"	Location/Qualifiers	
7	249.6	14..9	959	106	AL537150	AL557150	1. . 878	
8	246.4	14..8	980	106	AL57181	AL557181	/strain="RAK"	
9	246.4	14..6	645	113	AW24051	AW224051	/db_xref="taxon:29729"	
10	243	14..6	645	113	AW23768	D40006 RIC10372A	/clone="GA_EB024G23f"	
11	239.4	14..4	716	156	AW23768	AW23768 EST300579	/clone="Gossypium arboreum 7-10 dpa fiber library"	
12	237.6	14..3	637	113	AW23768	AW398404 EST298251	/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"	
13	236.2	14..2	668	115	BFG17440	BFG17440 HYSMEC01	/lab_host="E. coli"	
14	233	14..0	772	151	AW130455	AW130455 PROVARCB3	/note="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XbaI"	
15	227.4	13..7	632	174	BG128308	BG128308 EST423954	/note="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XbaI"	
16	227.2	13..7	790	155	BG599254	BG599254 EST50154	/note="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XbaI"	
17	226	13..6	1351	167	BEB22296	BEB22296 HYM022CF.	/note="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XbaI"	
18	226	13..6	1351	219	A186676	A186676 EST241998	/note="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XbaI"	
19	225.2	13..4	825	138	BEG4218	BEG4218 MTSWIA13	/note="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XbaI"	
20	222.4	13..4	660	152	BE334888	BE334888 AL564550	/note="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XbaI"	
c	21	221.4	13..3	899	106	AL564550	AL564550	BASE COUNT ORIGIN
c	22	221.4	13..3	920	106	AL59862	AL59862	253 a
c	23	220.8	13..3	920	106	AL59862	AL59862	157 c
c	24	220.4	13..3	598	103	A1895994	A1895994 EST25437	219 g
c	25	219	13..2	710	174	BG128262	BG128262 EST423908	245 t
c	26	215.2	902	106	AL531904	AL531904	4 others	
c	27	214.4	12..9	817	152	BG344483	BG344483 HVSMBQ000	17
c	28	214.4	12..9	902	106	AL555787	AL555787	17
c	29	214.2	12..9	870	152	BG344720	BG344720 HVSMBQ001	17
c	30	214	12..9	890	105	AL514684	AL514684	17
c	31	212	12..8	787	155	BG594484	BG594484 EST433162	17
c	32	211.2	12..7	671	166	BE31897	BE31897 NE034C12L	17
c	33	211	12..7	879	105	AL560505	AL560505	17
c	34	210.8	12..7	710	163	BE316553	BE316553 L48-1652T	17
c	35	209.4	12..6	612	113	AW216317	AW216317 EST25531	17
c	36	208.8	12..6	629	149	BR473185	BR473185 WHE0922_F	17
c	37	208.8	12..6	715	155	BG592035	BG592035 EST429877	17
c	38	208.4	12..5	955	105	AL517839	AL517839	17
c	39	208.2	12..5	796	174	BG124348	BG124348 EST470110	17
c	40	207.4	12..5	739	118	AW622566	AW622566 EST313366	17
c	41	204.4	12..3	842	107	AU128717	AU128717 AU128717	17
c	42	204.2	12..3	926	106	AL53693	AL53693 AL53393	17
c	43	203.6	865	106	AL55977	AL55977	17	
c	44	203.2	12..2	857	105	AL532194	AL532194	17
c	45	201.8	12..1	637	155	BG600875	BG600875 EST50770	17
ALIGNMENTS								
RESULT 1	BF275584	BF275584	878 bp	mRNA EST	07-MAR-2001	CGCCAGGATTGTGTGTTAAAGCTATGGTGTGAGTCATCTTGACAGTG	840	
DEFINITION GA_Eb024G23f	arboeum cDNA clone GA_Eb024G23f	GA	mRNA sequence	EST fiber 1 library	Gossypium	841 CGCCAGGATTGTGTGTTAAAGCTATGGTGTGAGTCATCTTGACAGTG	387	
ACCESSION BF275584	arboeum cDNA clone GA_Eb024G23f	BF275584				842 CTCCGTTGTTGTGAAAGGAGAACGCTCTCTCAAGATTCGAGCTTG	388	
VERSION BF275584.1	EST.	GI:1120654				843 901 GTACAGTGTAGATGAGGATCTAGCTGTTAAAGCTACAGTCAGCTTG	900	
KEYWORDS Gossypium	Gossypium arboreum.					844 448 CTGAGTTCAAGCTAGTGTGTTGGCTGTTCTCGAGATTCGAGCTTG	507	
SOURCE Gossypium arboreum.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					845 961 GACAGGCTCTAGATGAGCTGTTAAAGCTACAGTCAGCTTGAGGAA	1020	
ORGANISM Gossypium arboreum.	Spermatophyta; Magnoliopsida; Eudicots; Malvales; Malvaceae; Gossypium.					846 508 509 510 511 512 513 514 515 516 517 518 519 520	567	
REFERENCE 1 (bases 1 to 618)	Rosidae; Eurosidae II; Malvales; Malvaceae; Gossypium.					521 522 523 524 525 526 527 528 529 530 531 532 533 534	1080	
AUTHORS Wind,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wikins,T.A.	An integrated analysis of the genetics, development, and evolution					535 536 537 538 539 540 541 542 543 544 545 546 547 548	1140	

FEATURES source		QY 724 AAGTCTTAACCAACCGTCATTACTCATATTCCAGATGATGGATGGTGA 779
		Fax: (613) 759-1701
		Email: singhjaleem.agr.ca.
		Location/Qualifiers
1 .977		/organism="Zea mays"
		/cultivar="CO228"
		/ab_xref="taxon:4577"
		/clone="Zm04_04909"
		/clone.lib="Zm04_AbRC_ECoRC_cold_stressed_maize_seedlings"
		/tissue_type="Leaf crown"
		notes="Vector: Bluescript SK-/XbaI EcoRI; Site_1: Eco RI; Site_2: Xba I; Lower temperature 50 C / hour from 22 to 120C; bring to 50 in 1 hour from 120C. Leave at 50C 2 days / photoperiod 16 hours. Light intensity was 125 uE-1 library prepared by in vivo mass excision from amplified
BASE COUNT	276 a 205 c 241 g 223 t 32 others	ORIGIN
ORIGIN		
Query Match	15.3%; Score 254; DB 152; Length 977;	
Best Local Similarity	56.7%; Pred. No. 2.3e-60;	
Matches	440; Conservative	
	23; Mismatches	
	310; Indels	
	3; Gaps	
	1;	
QY	7 GGCTTCATPTGCACAAAGAACATCAATTTCAGCAGTGCGCTGCGCTGCGCG 66	
Db	202 GGACAYATCGYGGAAAGACAGTCAGTTGTGTTGAGGCCGTCYCATTGTGAAGC 261	
QY	127 TTCTGAAAGAAGCTTGGTCTCTTAACTACTANTGAGGGTAAACCTTGTCAANG 186	
Db	322 TTATGAGCAAGCTTGTGCAACGAAAGTCAAGATGGTACTTTACGAAAGA 381	
QY	187 AGATGGAATAGAGATCATTTGAAACATGGAGCAATGGCTCAGAGGCT 246	
Db	382 GCATGAAATTAGGATAGACTAAAGAATGTTGTGCAAGCSTGTGAAACAGGTGTA 441	
QY	247 CTAAACCAATGATATGCGCTGATGGAGGACTACTGCCACAGTTGACACAGCA 306	
Db	442 ATGGWACYATGACATGCTCGCGATGTTACCATGKCCACTKTTGACAAAGCCA 501	
QY	307 TGTCTCATGAAAGGCAAAATGACAGCAGCAGTGTCAACATTGGTACCTCGAG 366	
Db	502 TATTGATGGGGTCAAATGTTGGAATKAATGCTATGATTAAAGGGTG 561	
QY	367 GCATGAAACACCAACAGCACAGCTGTTGAGCTCGAACCCATTGTCACCTGT 426	
Db	562 GAACATCATTGGCTGTGAGCTGTGTRACCATCTTAARGCATGCCAGATAKCA 621	
QY	427 CTGGCAAGAACCTATGCGAGGCGCAGATATCAGCTGAA - AAGTG 493	
Db	622 GCATCTCAGAAATGCAAGCTGCAAGTATATCGGCTGAA - AAGTG 681	
QY	484 GAGGATATCTCAGAACCTGAGCTGAGGCTGGGGCAAGGAGTGTGATTAACCATCGAA 543	
Db	682 GTGAGCCTATGCCAACGGCTGTGAGGAGTGTGAAACCCATTTGGGG 741	
QY	544 AATCTCGAGGTATGGAACGAACTGAAAGTGTGAGGATGCAATTGGACCGTGT 603	
Db	742 ACCTGTAACCCCTTTATAAAGGCTTGTGAGCTTGTGAGGGTAACTAGAGARSP 801	
QY	604 ACCGTCTCAATACATGGTACAGCAATGAAAGATGGTGCAGACCTGAAACCCATTTGGGG 663	
Db	802 ACATCTCCTGFACTCTTACCAACCCAAACCCAGAAATGTGAATGGAGACBGA 861	
QY	664 TTACTCTAATCAGGTAAGAAGTGTCAACATCCAGAGATTTGCAACTACTGTGAG 723	
Db	862 TGTGCTTAAATCATGACAAGAAGGGAGGACATGCTCTGKTTAGGTTAGAA 921	
BASE COUNT	306 a 188 c 242 g 251 t 1 others	ORIGIN
ORIGIN		
Query Match	15.3%; Score 253.4; DB 106; Length 988;	
Best Local Similarity	57.1%; Pred. No. 3.4e-60;	
Matches	500; Conservative	
	0; Mismatches	
	371; Indels	
	4; Gaps	
	2;	
QY	18 GCAAGAAATCAAAATTCCAGAGATGCGGGTGTGCCATGTTGGGGTATGATG 77	
Db	115 GCAAGATATAATTGGCTCAGATGCCAGCCTTAATGTCAGGGTGTGACCT 174	
QY	78 TTACGATACCGTCGAAGTAGCTGTGCTTAAGGGCAAGTGTGTTGAA 137	
Db	175 TTAGCGCATCTGCGCGTGTACAATGGCCAAAGGGAGACAGGTATGAGCAG 234	
QY	138 GCTTGTGTTCTCCATTACTAATGAGGGTAAACCATGCTAAAGAGATGCCATTA 197	
Db	235 AGTCGGGAATGCCAAAGTACAAAGATGGTGTGAGCTGTCAGATGCAATGACTTA 294	
QY	198 GAGATCATTGAAAGATGGGAGGAATGGTGTGCAAGTGGTCTAAGTGGTCTAAACCAAT 257	
Db	295 AAAGATAATACAAACATGGACTAACTTGTCAAGAGTGTGCAATACAAAT 354	
QY	258 GATATGCTGTGAGGGACGACTACTGCAACAGTTGTGACAGCAAGCATGTCATGAA 317	
Db	355 GAAGAGCTGGGTGCACTACACTGCTGACTCTGTCGCGCCTATAGCCAGGA 414	
QY	318 GAACTAAAATGTGACAGCAGGGTCAATCAATTGGTATCGTCGAGGCAATGAA 377	

RESULT	6	LOCUS	BF627437	811 bp	mRNA	EST	21-FEB-2001	
DEFINITION			HVSMED004N18F	(dehydration stress)	Hordeum vulgare seedling shoot EST library			
ACCESSION			BF627437					
VERSION			BF627437.2					
KEYWORDS			EST					
SOURCE			Hordeum vulgare					
ORGANISM			Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum					
REFERENCE			1 (bases 1 to 811)					
AUTHORS			Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Friesch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Sasaki, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.					
TITLE			development of a genetically and physically anchored EST resource for barley genomics					
JOURNAL			Unpublished (2000)					
COMMENT			On Dec 19, 2000 this sequence version replaced gi:11891595.					
Contact:			Wing, R.A., Clemson University Genomics Institute					
Clemson University			100 Jordan Hall, Clemson, SC 29634, USA					
Tel:			864 656 7268					
Fax:			864 656 4293					
Email:			rwing@clemson.edu					
Seq primer:			ANTAACTCTACTTAAAGG					
FEATURES		source	High quality sequence stop: 796.					
			1..811					
			/organism="Hordeum vulgare"					
			/cultivar="Morex"					
			/db_xref="taxon:4313"					
			/clone="HVSMED004N18F"					
			/clone_id="Hordeum vulgare seedling shoot"					
			/tissue_type="Seedling shoot"					
			/lab_host="TIC121"					
			/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XbaI"					
BASE COUNT	236	a	166	c	229	g	180	t
ORIGIN								
RESULT	7	LOCUS	AL515579	1017 bp	mRNA	EST	13-FEB-2001	
DEFINITION			AL515579_1	LTI_NFL011_NBC1	Homo sapiens	cDNA clone	CS0002YD20	5
ACCESSION			AL515579					
VERSION			AL515579.1					
KEYWORDS			EST					
SOURCE			human.					
ORGANISM			Homo sapiens					
REFERENCE			Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
			1 (bases 1 to 1017)					
AUTHORS			Li, W.B., Gruber, C., Jesse, J. and Polayes, D.					
JOURNAL			Full-length cDNA libraries and normalization					
COMMENT			Unpublished (2001)					
Contact:			Genoscope - Centre National de Séquençage					
Genoscope			BP 191 9106 EVRY Cedex - France					
Email:			Sequen@genoscope.cns.fr, web : www.genoscope.cns.fr.					
FEATURES		source	Location/Qualifiers					
			1..1017					
			/organism="Homo sapiens"					
			/db_xref="taxon:9606"					
			/clone="CS0002YD20"					
			/clone_id="LTI_NFL011_NBC1"					
			/sex="male"					
			/tissue_type="neuroblastoma cells"					
			/lab_host="DH10B"					
			/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang, Life Center Drive Rockville Maryland 20850, USA. Fax : (1) 301 610 8571 Email : fliang@lifetechnologies.com URL : http://fulllength.invitrogen.com" 2 others					
BASE COUNT	308	a	191	c	255	g	261	t
ORIGIN								
Query Match	15.0%		Score 249.6;	DB 105;	Length 1017;			
Best Local Similarity	56.8%		Pred. No. 4e-59;					

	Matches	478; Conservative	1;	Mismatches	360; Indels	3;	Gaps	1;
OY	18	GCAAGAAATCAATTTCAGCAGATCGGCCGCGCCATGGCGGGAGTTGATAG	77					
Db	116	GCCAAGTGTAACTTGGTGCGATGCCGAGCCTTAATGCTTCAGGTAGACCT	175					
OY	78	TTCAGCATACCGTAACTAAGCTTGGCTTAAGGGCCTATGTTGAA	137					
Db	176	TTCAGCATACCGTAACTAAGCTTGGCTTAAGGGCCTATGTTGAA	137					
OY	138	GCTTGTGTTCCCTTAATTAATGACGGGAACTTGTCAAGAGATCGATA	197					
Db	236	ACTGGGAACCTCCAAACTAACAAAGATGTTGACTGTCAGTCATTCTA	295					
OY	198	GAGATCATTTGAAACATGSGAGCAATTGGCTGAAGTGCTCAAACCAAT	257					
Db	296	AAAGATAATACAAACAAACATTGGCTAACTTGTCAAGATGTTGCAAAAT	355					
OY	258	GATATGCTGGTGTGGCAGCATACTCCAACTTGTCAACAGATGTTGAA	317					
Db	356	GGAGAGCTGGGGACTACACGCTACTACGGCACGGCTATAGCGGAGGA	415					
OY	318	GGACTAAATGAGCAGCAGTGTAACTTGTGAGGCGATGAA	377					
Db	416	GGCTTGAGAGATGTAGCAAAAGGTGCTAACTCAGTGAATGAGTGA	475					
OY	378	GCAACAGCACACGCTGTGAGCATACAGCTGTCACCTGTGCAAGGAA	437					
Db	476	GCTGTGTTGCTGTTGAACTAAAGGAGCTAACCTGTGACCAACCCGAA	535					
OY	438	GCTATGTCAGCTGCTGAGTATGCAACCTGTGCAACCTGTGCAAGGAA	494					
Db	536	GAATTCAGCAGTTGCTAGTTCTGCAACAGGGAGAACAGATTCATC	595					
OY	495	TCAAAAGTATGGCTGGCGACGATGGTGTATTACATGGAAATCTGGGT	554					
Db	596	TCTATGCAATTAACAAAGTTGAGAAGAGGGTCATCACAGTAAGATGAA	655					
OY	555	ATGAAAGAACACTTAAAGGGTGCAGGCAATTGGCTGTTACCTGCAA	614					
Db	656	CTGATGATGATGAACTTGTAGCTGAACTTGTGAGCTGATGTTGATCC	715					
OY	615	TACATGGCAGACAGATGAAATGGTGCAGACCTGAAACACCATTATCATC	674					
Db	716	TACTTAAATACATCAAAAGGCTGAAATGTTGATTCAGGATGCTATTC	775					
OY	675	ACGGATAAAAAGTCACACATCCAGACATTGCCACTACTTGAGAAGTC	734					
Db	776	AGTGAAGAAGAAATTCTCTAGTATCCATCCATTGACCGCTCTGAA	835					
OY	735	ACCAACCGTCATTCTCATATGCGATGATGGATGGTAGAGACTCCACCT	794					
Db	836	CACGGTAACGCTTGTCTATGCGAGATGTTGAGGCTTGTGAA	895					
OY	795	GTCTGAAACAGATGCTGACTTCATGTTGCTGTCAGGCCAGATTG	854					
Db	896	GTCTGAAATAGCTAAAGGTGTCTCACTGTTGGCTAGTAAAGGCCAGGT	955					
OY	855	GA 856						
Db	956	GA 957						
RESULT	8							
AL557150 LOCUS	AL557150	959 bp mRNA sequence.	EST	16-FEB-2001	1			
DEFINITION	AL557150 LTI_Fl012_TCI	Homo sapiens	cdna clone	CS0DH002YB12	5			
ACCESSION	AL557150		prime					
VERSION	AL557150.1	GI:12900476						
KEYWORDS	human.							
SOURCE								
ORGANISM		Homo sapiens						
FEATURES	source							
	1. 959							
	/organism="Homo sapiens"							
	/db_xref="txon:9506"							
	/clone="CS0DH002YB12"							
	/tissue_type="T cells from T cell leukemia"							
	/lab_host="DH10B"							
	/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned, into the Not I and Eco R sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email: fliang@lifetech.com URL : http://fulllength.invitrogen.com" 1 others							
BASE COUNT	291	a	238	g	246	t	1	others
ORIGIN								
Query Match			14.9%					
Best Local Similarity			56.7%					
Matches	477;	Conservative	1;	Mismatches	361;	Indels	3;	Gaps
								1;
OY	18	GCAAAAGAATCAATTTCAGCAGATGGCTGCTCCCAATGGGGAGTTGATG	77					
Db	118	GCCAGATGCTAAATTGGCTGAGTCAGTGCTGAGCTTAATGCTCAAGGTGAGACCT	177					
OY	78	TTCAGAGATCGCTAACAGTGTGCTGAGCTTGTGAGGCTTGTCTGAA	137					
Db	178	TTCAGCTGCTGGCCGTTACATGGGCTAACAGGAGAACAGTGTATGGAGCG	237					
OY	138	GCTTGTGCTCCCTTAATCTCATATGCGATGATGGATGGTAGAGCTCCACCT	197					
Db	238	AGTGGGAAGTCCCAGTACAAAGATGGTGTGCTGAGTCATTGACTTA	297					
OY	198	GAATGATTTGAAACAGTGGGACAAATGGCTGAGTGGCTTGTCTGAA	317					
Db	298	AAAGATAATACAAAGGCTGAACTTGTGAACTTGTGCTAACACATGCA	417					
OY	318	GTATGCTGCTGAGCTTGTGAGCTTGTGCTGAGCTTGTGCTAACACATGCA	377					
Db	418	GCCTGAGGAGTACAGTGTGAACTGCTGAGCTTGTGCTAACACATGCA	477					
OY	378	GCAACGCAACAGCTGCTGAGCTTGTGAACTGCTGAGCTTGTGCTAACACATGCA	437					
Db	478	GCTGTGATGCTGAACTGCTGAGCTTGTGCTAACACATGCA	537					
OY	438	GCTATGCTGAGCTTGTGCTAACACATGCA	494					
Db	538	GAATGCTGAGCTTGTGCTAACACATGCA	597					
OY	495	TCAAGAGCTGAGCTTGTGCTAACACATGCA	554					
Db	598	TCTGATGCTGAGCTTGTGCTAACACATGCA	657					
OY	555	ATGGAAACAGACTGAGCTGAGGCTGAGCTTGTGCTAACACATGCA	614					

RESULT 9

Db 658 CTGAATGTAATTAGAATTATTGAAAGCATGAAAGTTGATCGAGGCTTATTCCTCA 717
 Qy 615 TACGTGGTACAGACATGAAATGTTGAGACCTTAAACCCATTACTTATTC 674
 Db 718 TACTTATTATACATCAMAAGGTCAGAACTGTAAGTCCAGGATGCCCTTGCTG 777
 Qy 615 ACGGATAAAAAGTGTCAACACATCCAGAACATGCAAGCATTGGTCACTACTTGAGGAGTCTPAA 734
 Db 778 AGCGAAGAGAAATTCTGTAATGCACTGCAGTCAGTGTACTCTCTCTGAATGCAATGCT 837
 Qy 735 ACCAACCGCCATTACTCTTATGCGATGATGTTGAGACTTCACCCCT 794
 Db 838 CACCGTAGCTTGTCTAATPGCTGAGATGTGAGCTGAGTCATGACTC 897
 Qy 795 GCTTGAACAGATPGTGTGACTTTCATGTTGTCAGAACGCCAGATTGGT 854
 Db 898 GCTTGAATAGCTAAAGTTGGCTCAGGTGTGGCACTYAGGCTCCAGGTTGGT 957
 Qy 855 GA 856
 Db 958 GA 959

RESULT 9

Db AL557181 980 bp mRNA EST 16-FEB-2001 prime
 LOCUS AL557181 LTI_FL012_TCl Homo sapiens cDNA clone CSODH002YD16 5 prime
 DEFINITION mRNA sequence.
 ACCESSION AL557181
 VERSION AL557181.1 GI:12900537
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope - Centre National de Sequençage
 BP 191 91006 ERY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES source

ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 980)
 AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 CONTACT Genoscope - Centre National de Sequençage
 BP 191 91006 ERY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES source

ORGANISM Homo sapiens
 /clone_id="LTI_FL012_TCl"
 /tissue_type="T cells from T cell leukemia"
 /lab_host="DHIOB"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI-I and Eco RI sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies & division of Invitrogen 9800 Medical center Drive Rockville, Maryland 20850, USA Fax : (301) 610 8371 Email : liang@lifetech.com URL : http://fulllength.invitrogen.com"
 BASE COUNT 304 a 185 c 241 g 248 t 2 others
 ORIGIN

RESULT 10

Db 172 TTACCGAATCTGGCCCTTACAATGGGCCAAGGAAACAGTATGACAG 231
 Qy 138 GCTTGGTCTCCCTTAACTATGAGGGSTAACCATGCTAAAGATGCAATT 197
 Db 232 AGTGGGGAGTCCAAAGTACAAAGATGGGCTGACTGTCAGTCATGACTA 291
 Qy 198 GAAGATCATTTGAAACAGTGGGCAAAATTGGTGTCTGAGTSGCTCTAACCAT 257
 Db 292 AAAGATAATTACAGACATGGCTAACTGCTGAGTGTGCCATTACACAAAT 351
 Qy 258 GATATGCTGGTGTGGAGCAACTACTGCAACAGCTTGTGACATGCAA 317
 Db 352 GAAGAGCGGGATGCACTACACTGCTACTGTACTGGCACCTATGCCAAGGAA 411
 Qy 318 GGACACAGAACATTGACAGCAGGCTAACTCCATGTTGACATGCCGAGGAGGTGATGTA 471
 Db 412 GGCTTCAGAGAATTGACAGGCTAACTCCATGTTGACATGCCGAGGAGGTGATGTA 437
 Qy 378 GCAACAGCACAGCTGTTGAGCCUTGAGGCTAACTTCACTGGAATCAGGAGAGAA 377
 Db 472 GCTCTGGTGTGGCTATTGCTGACTTAACTGCTCTCACCTGTCACCCCTGA 531
 Qy 438 GCTATGCTGAGTCGCTGAGTACATCACCTCTGAAAGA---TGGAGATATC 494
 Db 532 GAATTGCAAGCTGCTAGATTCCTGCAACGGAGAACAAATTGCTATGTC 591
 Qy 495 TCAGAAGTATGGGGTGACCATGGTGTATTACACATGAGAATCTCAGGT 554
 Db 592 TCTATGCAAGAAAGATGGAGAAGAAGGCTGATCACAGTAAGGATGAAACA 651
 Qy 555 ATGGAAAGAGAATCTGAGGCTGAGGCAATTGACCTGTGTTACCTGTCAA 614
 Db 652 CTGATGTTGATGAAATTGAGCTGAGGCTGAGGCTGAGTTCAGGATTTTC 711
 Qy 615 TACATGGTACAGACATGAAAAATGTTGAGACCTTGAAACCATTATCTTAATC 674
 Db 712 TACTTATTATACATCAMAAGGTCAAGAATGTAATTCAGGATGCCCTATGCTGTG 771
 Qy 675 ACGGATAAAAAGTGTCAACACATCCAGACATTGGCACTACTGTGAGAATCTAA 734
 Db 772 AGTGAAGAGAAATTCTGATGTTGAGCTGAGTGTGAGCTGAGTGTGAGTGT 831
 Qy 735 ACCAACCGCCATTACTCTTATGCGATGATGTTGAGGGACTTCACCCCT 794
 Db 832 CACCGTAGCCUTGTCATAATGCGAGAATGTTGAGCTGAGGCTTAAGTACCTC 891
 Qy 795 GCTTGAACAGATPGTGTGACTTTCATGTTGTCCTCAAGGCCAGGATGTT 854
 Db 892 GCTTGAATAGCTAAAGTTGGCTCAGGTGTGGCAGTCAGGCTCAAGGTTGGT 951
 Qy 855 GA 856
 Db 952 GA 953

RESULT 10

Db AW224051 645 bp mRNA EST 07-DEC-1999
 LOCUS AW224051 tomato red ripe, TAMU Lycopersicon esculentum cDNA
 DEFINITION EST00852 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
 ACCESSION AW224051
 VERSION AW224051.1 GI:6535735
 KEYWORDS EST
 SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 REFERENCE 1 (bases 1 to 645)
 AUTHORS Alcalá,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.

Query Match 14.8%; score 246 4; DB 106; Length 980;
 Best Local Similarity 56.5%; Pred. No. 3..le-58;
 Matches 476; Conservative 1; Mismatches 362; Index 3; Gaps 1;

Qy 18 GCAAAAGAGAAATTCAGCAGATGGCGCTCTGCCATGGGGGGTGTATG 77
 Db 112 GCCAAGATGTTGAGCTGAGTCAGTCAGGCTTAATGCTTAAGGGTAGACCT 171
 Qy 78 TTACAGATACGGTCAAGTACAGTACGGTTGCTCAAAGGCCAATGCTGCTGAA 137

BASE COUNT 204 a locales were discarded prior to freezing the pericarp.
 ORIGIN

910 TTTAGGAGGATCTAGACTGAAATTAAAGATGCTACATGACGCCCTGGCAGGTG 969
 365 TCGGGGTGAGTGGCTCACTTGACAGCACAAATCAGTTAGGACGGTG 424
 Db 425 CAAAGTGGCTTACAGAACGTCACAGCATTTGTTGAGCCATACAGGAG 484
 QY 430 CTATGCTTAACGTTGACTATTAACTCAATTAGAACACAATCTGACTTG 1089
 Db 485 AATGACTAAGGGTGGACAAATAAAATCTCATCGAGCTCCGACAGAATACG 544
 QY 1090 ATCGTGAAGAACATCAAGACGTTGGCAAACTGCTGGTGTGAGTCAG 1149
 Db 545 AGAGGAAACCTCATGAGGATGCAACCTGCTGGTGTGAGTCAG 604
 QY 1150 TAGGAGTCCACAGACAGACTTAAAGAAATGAACTCGATTAGGAGCTAA 1209
 Db 605 TGGGACACACAGACAGACGCAACTAAGAGAGAGTGTGAGTGGAGG 664
 QY 1210 ATGCTACACGTCACCGCTGAGAAGTGTCTGGTGTGAGG 1255
 Db 665 ATGCTACCAAGCTCTGTGAGGAAGTATTGTGTGGAGG 710

RESULT 12

AW23768

LOCUS AW23768 637 bp mRNA EST 07-DEC-1999
 DEFINITION EST0059 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
 ACCESSION clone CLEN13H9, mRNA sequence.
 VERSION AW23768. 1 GI:6535452
 KEYWORDS EST.
 SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopericon.
 REFERENCE (bases 1 to 637)
 AUTHORS Alcalá,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
 Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ann,S., Ronning,C.M.,
 Fraser,C.M., Martin,G.B., Tankley,S.D. and Giovannoni,J.
 TITLE Generation of ESTs from tomato fruit tissue
 unpublished (1999)
 COMMENT Contact: David Frisch
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 4366
 Fax: 864 656 4293
 Email: dfrisch@CLEMSON.EDU

FEATURES

source

Location/Qualifiers

1. -637 /organism="Lycopersicon esculentum"
 /cultivar="TM496"
 /clone="CLEN13H9"
 /db_xref="Taxon:4081"
 /clone.lib="tomato fruit red ripe, TAMU"
 /tissue_type="pelican"
 /dev_stage="red ripe (7-20 days post-breaker)"
 /note="Vector: plasmid; Source: ECR1; Site-1: ECR1; Site-2: Xhol; supplier: Giovannoni; Fruit were tagged at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit) and harvested 7 days post-breaker (fully ripe); 10 days post breaker, and 20 days post-breaker (over-ripe); 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and

5 prime sequence.

AW23768

LOCUS AW23768 637 bp mRNA EST 07-DEC-1999
 DEFINITION EST0059 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA clone CLEN13H9, mRNA sequence.
 ACCESSION AW23768. 1 GI:6535452
 KEYWORDS EST.
 SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopericon.

REFERENCE (bases 1 to 668)
 AUTHORS Alcalá,J., Vrebalov,J., White,R., Matern,A.L., Lakay,J., Holt,I.E., Liang,F., Hansen,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fujii

Query Match 14.3%; Score 237.6; DB 113; Length 637;
 Best Local Similarity 50.8%; Pred. No. 8.1e-56; Matches 387; Conservative 0; Mismatches 249; Indels 0; Gaps 0; Gaps 0;

QY 607 TTCTCTAACTACATGACAGCATGAAAGTGGCAGACACCTTGAACATTA 666
 Db 2 TCTCTCTTACTTGTGACGACTGAGAATGAGTCGATGAGACAGCTAANT 61
 QY 667 TCTTATCAGGATAAAAGGTCAACATCCAGACATTTGGCCTACTTAGGAG 726
 Db 62 TCTCTGTGTTGATAAAGATAACATGACAGAGTCTGTTATGCTCTGGAGG 121
 QY 727 TTCTTAAACCCACCGTCATCTACATATTGAGTGGTGGAGACACTTC 786
 Db 122 CTATCGAGAAATGTTACCCATTAAATTATTATTCTGAGATTTGKCGAGAACGCTTG 181
 QY 787 GAACCTTGTGCTGACAGAGTCTGAGTGGCTTGAAGTGTGTTGTAACAGGCAG 846
 Db 182 CAACCTCTGTTGCTATAGCTTGTGAGGCTCTGAGTCGCTGACTTAAGCTCTG 241
 QY 847 GATTTGGTATCTGCTGTAAGCTGTTGAGTGGCTTGAAGTGTGTTGAGTGTGAG 906
 Db 242 GTTGGGAGGAAAAGCCGATCTGATGATGATGATGACACCTTACTGGAGGACT 301
 QY 907 TGATACAGAGCTCTAGACTTGATTAAGATGCTACATGACGCCCTGGACAGG 966
 Db 302 TTATAGGGAGCTGGCTTACTTGACAGGTGAGGAGTCTGGTCAG 361
 QY 967 CTGCTAAGTACAGTGTAGATAAGATAGACAGACATGCTATCTGAGCAGTCAAGT 1026
 Db 362 CTGCTAAGTGTGCTACTAGGTGCCACTACATGTTGGTGTGAGTCCTCAG 421
 QY 1027 AAGCTTATTCTAACGTTGACTGATTAAGCTGCTACATGACACAAACTCTCTACT 1086
 Db 422 AGCGCTCACACAACTGTTGACAGTAAACCTGATAGAGGCTTCAGAGTCAG 481
 QY 1087 TTGACCGTGAAGAACCTCAGACGCTTGGGGAATTAGCTGCTGCTGAGCTTATCA 1146
 Db 482 ATGAAAGGAAAGCTTAACTGAAAGTGTCTAGTATCAGGGTGTGCTCATAC 541
 QY 1147 AAGAGGAGCTCAAGAAGACGCTTAAAGAAATGAACTGTGCTTGGAGTC 1205
 Db 542 AGGTGGACCTTAACTGAAGTGTGAGGAGAACCTAGAGTAGAGATGCTC 601
 QY 1207 TAATGCTACAGTGTGAGGAGAACCTAGAGTAGAGATGCTC 1242
 Db 602 TCAATGCAACAAAGGAGCTGTGAGGAGGTATG 637

RESULT 13

AW398404

LOCUS AW398404 668 bp mRNA EST 07-FEB-2000
 DEFINITION EST298251 L. pennellii trichome, Cornell University Lycopersicon pennellii cDNA clone CLP615 similar to similar to nearly identical to Solanum tuberosum chaperonin-60 beta subunit, mRNA sequence.
 ACCESSION AW398404
 VERSION AW398404. 1 GI:6916874
 KEYWORDS EST.
 SOURCE
 ORGANISM Lycopersicon pennellii
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopericon.

REFERENCE (bases 1 to 668)
 AUTHORS Alcalá,J., Vrebalov,J., White,R., Matern,A.L., Lakay,J., Holt,I.E., Liang,F., Hansen,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fujii

Db	544	ATTAAACCTGATAGGGCTGCAGATCAAGATTTGAAAGGAAGCTAAATGAA	603
Qy	1113	TTCGCGAATTCGTTGAGCTTGTGTTAGCTTCAAGTAGGCTCCACAGAGCT	1172
Locus	ATTCTTAAGTATCAGGAGGCTGCTGTACAGGCTCAAACGTGAAACTGAA	663	
Db	604	ATTCTTAAGTATCAGGAGGCTGCTGTACAGGCTCAAACGTGAAACTGAA	663
Qy	1173	TTAA	1177
Db	664	TTGA	668
RRESULT	14		
BR617440			
LOCUS	BR617440	772 bp	mRNA
DEFINITION	HVSMEC017F22f	Hordeum vulgare seedling shoot EST library	EST
ACCESSION	HVSMEC0003	(Etiolated and unstressed) Hordeum vulgare cDNA clone	
VERSION	BR617440		
KEYWORDS	BR617440.2	GI:13108972	
SOURCE	EST		
ORGANISM	barley.		
Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; Pooidaeae; Triticeae; Hordeum.			
REFERENCE	1	(bases 1 to 772)	
AUTHORS	Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J.B., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.		
JOURNAL	Unpublished (2000)		
COMMENT	On Dec 18, 2000 this sequence version replaced gi:11881174.		
Contact:	Wing RA		
Clemson University Genomics Institute			
100 Jordan Hall, Clemson, SC 29634, USA			
Tel:	864 656 7288		
Fax:	864 656 4293		
Email:	rwing@clemson.edu		
Seq. Primer:	ATTAAACCTGATAGGG		
High quality sequence stop:	719.		
FEATURES			
source			
1.	772		
/organism="Hordeum vulgare"			
/cultivar="Mortex"			
/db_xref="taxon:4513"			
/clone="HVSMEC0017F22f"			
/clone_id="Hordeum vulgare seedling shoot EST library			
HVSMEC0003 (Etiolated and unstressed)"			
/tissue_type="Seedling shoot"			
/lab_host="JUCC21"			
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XbaI;"			
BASE COUNT	235 a	152 c	214 g
ORIGIN	171 t		
Query Match	14 0%	Score 233;	DB 151;
Best Local Similarity	57.9%	Pred. No. 1: 1e-54;	Length 772;
Matches	413;	Conservative	0;
		Mismatches	300;
		Indels	0;
		Gaps	0;
Qy	478	AAGTGGAGGATRATCTCGAGAGCTATGGGCCGTTGGGAAACGATGGTGTGATTC	537
Db	37	AAATCGGTAACATATGACAGGCTATGACCAAGGTTGGCGGAAGGAGCTGTTACCC	96
Qy	538	TGAGAAGATTCGGATGAGAACAGCTGAGCTGAGGCTGAGGCTGAGCTGATTC	597
Db	97	TTGAAGAGGGGGAGGTTCCGAGAACATCTTATGTTGAGGAGTGCAGTTGAGC	156
Qy	598	GGGGTACCTGTCATAATACATGTCACAGACATGAAATGGTGTGAGCTGAA	657
Db	157	GTGGTATCATCTACATTTATGTTGAGGCTGAGCTGAAATCACCGCTGAGC	215

Qy

658 ACCCATTACTTATCAGGGTAAAGTGCAACATCCAGAGATTGCCACTAC 717

Db

217 ACTGCAAGCTGCCTTGTGCAAGAAAATCACCAAGGACCGGACCTTATCAATGTC 276

Qy

718 TTGAGGAAGCTCTAAACAAACCGTCCATACTCATTTGAGATGATGGATGGTG 777

Db

277 TGGAGGAACCATAGGGTCAATACCCAATCCGATCATGTCGAGGATATTGAGCAGG 336

Qy

778 AAGCACTCAGACCTGCTGAGAAGGTTGGTACTTCAGTGGTACATGCTGGTCA 837

Db

-337 AGGCCTCTCAACCTGTTGCAACAGGTTTGGAAATCTGCTGATCA 396

Qy

838 AAGCCCAAGATTGGTGTGTAACACTGCTGAGAGATGCTACTGAGACATGACAG 897

Db

397 AAGCCCTGTTGGTGGAGGAGCAACCCAGTCTGAGACATGCTACTGAGACATGACAG 456

Qy

898 GTGGTACAGTGTACAGGAGCTAGGACTTGTGATTAAGAGATGCTACATGACGCC 957

Db

457 GAGGAACTGTTACAGAGACGGTGGACTCACAGTACAGTACAGGAGATACAGTC 516

Qy

958 TTGGACAGCTGCTAACATACAGTGTAGATAAGATAGCACAGTAATGTTGAGSTTCG 1017

Db

517 TAGGAGCCTGCAANGCTTCCTACAAAGTCGACACAACTAGTGTGTTGGCA 576

Qy

1018 GAAGTTCAAGCTATGCTACCTATGACAGTAAATGCAATTAGAACACAA 1077

Db

577 GCACCAAGGAGAGTGTGACTAAGAGGTTCACAGATCAAATCTCATGAGGTAGCAG 636

Qy

1078 CTCTCTGACTTGTGCGTAAACATACAAGAACGTTGGGAAATAGCTGCTGTTGGT 1137

Db

637 ACCAGACTACGGAGGAAACACTCAATGAAAGATGCAAGCTGCGGGGGGGTG 696

Qy

1138 CTGTTATCAAGTAGGGCTCAACAGACACACTTAAAGAAATGAACTT 1190

Db

697 CTGTTATCAAGGGAGCACACAGACACTGACTTAAGGAGAAAGTT 749

RESULT

15

AW330455

LOCUS AW330455 680 bp mRNA DEFINITION Ivermectin (SAW98PF-OvAF) Onchocerca volvulus adult female cDNA following PROVARCB31_5, mRNA sequence.

ACCESSION

AW330455

VERSION AW330455.1

KEYWORDS EST

ORGANISM Onchocerca volvulus.

REFERENCE 1 (bases 1 to 680)

AUTHORS Fischer, P. and Williams, S.A.

TITLE Genes Expressed in adult female stage of Onchocerca volvulus following treatment with ivermectin

JOURNAL Unpublished (1999)

COMMENT Contact: Peter Fischer

Molecular Parasitology

Bernhard Nocht Institute for Tropical Medicine

Bernhard-Nocht-Strasse 74, 20359 Hamburg, Germany

Tel: +49 40 42818 486

Fax: +49 40 42818 400

Email: Pfischer@biu.uni-hamburg.de

Seq primer: pBlueScript SK+

FEATURES source

/organism="Onchocerca volvulus"

/db_xref="taxon:6282"

/clone="PROVARCB31"

/clone_id="Onchocerca volvulus adult female cDNA following ivermectin (SAW98PF-OvAF)"

/sex="female"

/dev_stage="adult"

/dev_stage="adult"

/lab_host="X11-Blue MRF"
 /note="vector: lambda Uni-ZAP XR; site_1: Eco RI; site_2:
 Xho I; Filarial nematode parasite of humans. Two adult
 female worms of *Onchocerca volvulus* were isolated from
 one consenting patient from western Uganda. The patient
 was treated 28 hours and 7 month before nodulectomy with a
 single dose of 150 mg/kg ivermectin. Adult female worms
 were quick frozen. Their mRNA was converted to
 double-stranded cDNA using reverse transcriptase and
 oligo(dT) followed by RNase H and DNA pol I. The library
 has 2.9 x 10E5 independent recombinants and the average
 insert size is ~800bp. The library was constructed by
 Peter Fischer with worms provided by Dr. Dietrich W.
 Williams (U.S.A.) or dr. Peter Fischer (Germany), email:
 Williams@genomesmith.edu, Fischer@biu.uni-hamburg.de

BASE COUNT 230 a 93 c 151 g 204 t 2 others
 ORIGIN

Query Match 13.7%; Score 227.4; DB 114; Length 680;
 Best Local Similarity 61.2%; Pred. No. 6; 2e-53;
 Matches 385; Conservative 0; Mismatches 241; Indels 3; Gaps 1;

Qy 611 TCAATACATGATCTCAGCATGCAAAATGTTGCGACCTTGAAACCCATTATCTT 670
 Db 1 TCGTATTATTACATATGATGAAATGTTGGACCTATCTCT 60

Qy 671 ATTCAGGATTAAGATGTCACACATCCAGACATTGTCACACTTGGAGAGTC 730
 Db 61 ATTACAGGAAACAACTATATATTCACCCCTTGCTTCTTATTGTGAGCTGTGTT 120

Qy 731 TAACACCAACGGTCATRACTATATTGTCAGATGTTGGGTTGGAGGACTTCAAC 790
 Db 121 TAACTGGAAACCTTACTATCATGTCGAGACATGTTGGTAAAGCTTCAATGATAC 180

Qy 791 CCTTGCTTAAACAGATGTTGGTACTTCAATGGTGTGCTAACGCCAGGT 850
 Db 181 TTAGTGTATAATAGTGGTGGAGTCCTAAAGTGTGAGTGAAGCTCCAGGT 240

Qy 851 TGGTGTGGCTTAAGTGTGAGTCCTTCAATGTCAGATGCTTCAGTGTGAGTC 907
 Db 241 TGGTGTGAGAGAGGAGATCTTCAATGATAGTCAGCTTAACTATGCTAATGTT 300

Qy 908 GATTACAGAGATCTAGGACTGAATTAAGAGGCTCAAGACGCCATTGGACAGC 967
 Db 301 CATAAAAGGAGAACCTGGTAAATGGAGACCTCTCTGAGACCCATTGGCTC 360

Qy 968 TGCTAAGATTAAGCTGATAAGTAGCAGCTTGTGAGGTCTGAGCTCAGA 1027
 Db 361 TAAATGTTAAATCTACTAAGATACTTACATGTTAGGAAATAGTGTACTGA 420

Qy 1028 AGCTATGCAACCGTATGCACTGATTAATGCGAAATTGAAACACTCTGACTT 1087
 Db 421 CAGATTAAGCTGAGTAACTGGCAGATTAATCTCAATTGAGCTCTCACTCTGACTA 480

Qy 1088 TGACCTGAAACTCAGACGACTTGGGAATTACTGAGTGTGCTTGTGTT 1147
 Db 481 TGATAAAGGAAATTAGAGACGCTTGTGAAATATCAGGGTGTGTTCTA 540

Qy 1148 ATTAGGACTCCACAGAGACGCTTAAAGAAATGAACTCGCATGAGATGCTCT 1207
 Db 541 AGTTGCTGGAGACCTGTGAGTAAAGAACTGAAAGTAGGGTGTGCTGTT 600

Qy 1208 AATGCTTACGGTGGAGCTGAGAAGTGGTGTGAGAGATGGTGTGAGATGCTC 1236
 Db 601 GCACGCCACAGAGACTGCAATTGAGGA 629

Search completed: November 9, 2001, 10:10:35
 Job time: 3752 sec

Wed Nov 14 11:59:09 2001

us-09-001-737-7.rst